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Range: from to Features: ☐ SNP ☒ CDD ☒ MGC ☒ HPRD ☒ STS ☒ tRNA

☐ 1: P08887. Reports Interleukin-6 rec...[gi:124343]

BLink, Conserved
Domains, Links

Comment	Features	Sequence
LOCUS	P08887	468 aa linear PRI 07-FEB-2006
DEFINITION	Interleukin-6 receptor alpha chain precursor (IL-6R-alpha) (IL-6R 1) (Membrane glycoprotein 80) (gp80) (CD126 antigen).	
ACCESSION	P08887	
VERSION	P08887 GI:124343	
DBSOURCE	swissprot: locus IL6RA_HUMAN, accession P08887; class: standard. extra accessions: Q16202, Q53EQ7, Q5FWG2, Q5VZ23, created: Nov 1, 1988. sequence updated: Nov 1, 1988. annotation updated: Feb 7, 2006. xrefs: X12830.1, CAA31312.1, X58298.1, CAA41231.1, AK223582.1, BAD97302.1, AL162591.16, CAH72853.1, BC089410.1, AAH89410.1, S72848.1, AAC60635.1, A41242, 1N26A, 1N2Q_C, 1N2Q_D, 1P9MC xrefs (non-sequence databases): IntAct: P08887, Ensembl: ENSG00000160712, HGNC: 6019, MIM: 147880, LinkHub: P08887, GO: 0005576, GO: 0005896, GO: 0019899, GO: 0004915, GO: 0008283, GO: 0007166, GO: 0007275, GO: 0006955, InterPro: IPR002996, InterPro: IPR003961, InterPro: IPR003530, InterPro: IPR003599, InterPro: IPR007110, InterPro: IPR003598, Pfam: PF00041, Pfam: PF00047, SMART: SM00060, SMART: SM00409, SMART: SM00408, PROSITE: PS50853, PROSITE: PS01354, PROSITE: PS50835	
KEYWORDS	3D-structure; Alternative splicing; Direct protein sequencing; Glycoprotein; Immunoglobulin domain; Membrane; Polymorphism; Receptor; Signal; Transmembrane.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (residues 1 to 468)	
AUTHORS	Yamasaki, K., Taga, T., Hirata, Y., Yawata, H., Kawanishi, Y., Seed, B., Taniguchi, T., Hirano, T. and Kishimoto, T.	
TITLE	Cloning and expression of the human interleukin-6 (BSF-2/IFN beta 2) receptor	
JOURNAL	Science 241 (4867), 825-828 (1988)	
PUBMED	3136546	
REMARK	NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).	
REFERENCE	2 (residues 1 to 468)	
AUTHORS	Yamasaki, K., Taga, T., Hirata, Y., Yawata, H., Kawanishi, Y., Seed, B., Taniguchi, T., Hirano, T. and Kishimoto, T.	
TITLE	Molecular structure of interleukin 6 receptor	
JOURNAL	Proc. Jpn. Acad., B, Phys. Biol. Sci. 64, 209-211 (1988)	
REMARK	NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).	
REFERENCE	3 (residues 1 to 468)	
AUTHORS	Schooltink, H., Stoyan, T., Lenz, D., Schmitz, H., Hirano, T., Kishimoto, T., Heinrich, P.C. and Rose-John, S.	
TITLE	Structural and functional studies on the human hepatic interleukin-6 receptor. Molecular cloning and overexpression in HepG2 cells	
JOURNAL	Biochem. J. 277 (PT 3), 659-664 (1991)	
PUBMED	1872801	
REMARK	NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).	
REFERENCE	4 (residues 1 to 468)	
AUTHORS	Totoki, Y., Toyoda, A., Takeda, T., Sakaki, Y., Tanaka, A. and Yokoyama, S.	
TITLE	Direct Submission	
JOURNAL	Submitted (??-APR-2005)	

REMARK NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
TISSUE=Kidney

REFERENCE 5 (residues 1 to 468)
AUTHORS
CONSRM Human chromosome 1 international sequencing consortium
TITLE Direct Submission
JOURNAL Submitted (??-MAY-2005)

REMARK NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

REFERENCE 6 (residues 1 to 468)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
CONSRM Mammalian Gene Collection Program Team
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932

REMARK NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).
TISSUE=Lymph

REFERENCE 7 (residues 1 to 468)
AUTHORS Horiuchi,S., Koyanagi,Y., Zhou,Y., Miyamoto,H., Tanaka,Y., Waki,M., Matsumoto,A., Yamamoto,M. and Yamamoto,N.
TITLE Soluble interleukin-6 receptors released from T cell or granulocyte/macrophage cell lines and human peripheral blood mononuclear cells are generated through an alternative splicing mechanism
JOURNAL Eur. J. Immunol. 24 (8), 1945-1948 (1994)
PUBMED 8056053

REMARK NUCLEOTIDE SEQUENCE [MRNA] OF 313-365 (ISOFORM 2).

REFERENCE 8 (residues 1 to 468)
AUTHORS Cole,A.R., Hall,N.E., Treutlein,H.R., Eddes,J.S., Reid,G.E., Moritz,R.L. and Simpson,R.J.
TITLE Disulfide bond structure and N-glycosylation sites of the extracellular domain of the human interleukin-6 receptor
JOURNAL J. Biol. Chem. 274 (11), 7207-7215 (1999)
PUBMED 10066782

REMARK PARTIAL PROTEIN SEQUENCE, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.

REFERENCE 9 (residues 1 to 468)
AUTHORS Novick,D., Engelmann,H., Wallach,D. and Rubinstein,M.
TITLE Soluble cytokine receptors are present in normal human urine
JOURNAL J. Exp. Med. 170 (4), 1409-1414 (1989)
PUBMED 2529343

REMARK PROTEIN SEQUENCE OF 20-49, AND SUBCELLULAR LOCATION.

REFERENCE 10 (residues 1 to 468)
AUTHORS Yawata,H., Yasukawa,K., Natsuka,S., Murakami,M., Yamasaki,K., Hibi,M., Taga,T. and Kishimoto,T.
TITLE Structure-function analysis of human IL-6 receptor: dissociation of amino acid residues required for IL-6-binding and for IL-6 signal transduction through gp130
JOURNAL EMBO J. 12 (4), 1705-1712 (1993)
PUBMED 8467812

REMARK MUTAGENESIS.

REFERENCE 11 (residues 1 to 468)
AUTHORS Martens,A.S., Bode,J.G., Heinrich,P.C. and Graeve,L.
TITLE The cytoplasmic domain of the interleukin-6 receptor gp80 mediates its basolateral sorting in polarized madin-darby canine kidney cells
JOURNAL J. Cell. Sci. 113 (PT 20), 3593-3602 (2000)
PUBMED 11017875

REMARK FUNCTION.

REFERENCE 12 (residues 1 to 468)

AUTHORS Buk,D.M., Renner,O. and Graeve,L.
 TITLE Increased association with detergent-resistant membranes/lipid rafts of apically targeted mutants of the interleukin-6 receptor gp80
 JOURNAL Eur. J. Cell Biol. 84 (10), 819-831 (2005)
 PUBMED 16270750
 REMARK FUNCTION, AND SUBCELLULAR LOCATION.
 REFERENCE 13 (residues 1 to 468)
 AUTHORS Varghese,J.N., Moritz,R.L., Lou,M.Z., Van Donkelaar,A., Ji,H., Ivancic,N., Branson,K.M., Hall,N.E. and Simpson,R.J.
 TITLE Structure of the extracellular domains of the human interleukin-6 receptor alpha -chain
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (25), 15959-15964 (2002)
 PUBMED 12461182
 REMARK X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 20-344.
 COMMENT On or before Dec 27, 2005 this sequence version replaced gi:74754774, gi:74755342, gi:74757093, gi:106829.
 [FUNCTION] Part of the receptor for interleukin 6. Binds to IL-6 with low affinity, but does not transduce a signal. Signal activation necessitate an association with IL6ST. Activation may lead to the regulation of the immune response, acute-phase reactions and hematopoiesis.
 [FUNCTION] Low concentration of a soluble form of interleukin-6 receptor acts as an agonist of IL6 activity.
 [SUBUNIT] Hexamer of two molecules each of IL6, IL6R and IL6ST.
 [INTERACTION] Q9NZ08:ARTS-1; NbExp=1; IntAct=EBI-299383, EBI-299412.
 [SUBCELLULAR LOCATION] Type I membrane protein (isoform 1); basolateral membrane. Secreted (isoform 2).
 [ALTERNATIVE PRODUCTS] Event=Alternative splicing; Named isoforms=2; Name=1; Synonyms=Long; IsoId=P08887-1; Sequence=Displayed; Name=2; Synonyms=Short; IsoId=P08887-2; Sequence=VSP_001682, VSP_001683.
 [TISSUE SPECIFICITY] Isoform 2 is expressed in peripheral blood mononuclear cells and weakly found in urine and serum.
 [DOMAIN] The two fibronectin type-III-like domains, contained in the N-terminal part, form together a cytokine-binding domain.
 [DOMAIN] The WSXWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cell-surface receptor binding.
 [PTM] A short soluble form may also be released from the membrane by proteolysis.
 [SIMILARITY] Belongs to the type I cytokine receptor family. Type 3 subfamily.
 [SIMILARITY] Contains 1 fibronectin type-III domain.
 [SIMILARITY] Contains 1 Ig-like C2-type (immunoglobulin-like) domain.

FEATURES

source	Location/Qualifiers
	1..468
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
gene	1..468
	/gene="IL6R"
Protein	1..468
	/gene="IL6R"
	/product="Interleukin-6 receptor alpha chain precursor"
Region	1..19
	/gene="IL6R"
	/region_name="Signal"
	/experiment="experimental evidence, no additional details recorded"
Region	20..468
	/gene="IL6R"
	/region_name="Mature chain"
	/experiment="experimental evidence, no additional details recorded"
	/note="Interleukin-6 receptor alpha chain."
	/FTId=PRO_0000010895."
Region	20..365
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	/region_name="Topological domain"
	/inference="non-experimental evidence, no additional details recorded"
	/note="Extracellular (Potential)."
Region	22..23
	/gene="IL6R"
	/region_name="Beta-strand region"

Bond /experiment="experimental evidence, no additional details recorded"
bond(25,193)
/gene="IL6R"
/bond_type="disulfide"
/experiment="experimental evidence, no additional details recorded"

Region 26..112
/gene="IL6R"
/region_name="Domain"
/experiment="experimental evidence, no additional details recorded"
/note="Ig-like C2-type."

Region 32..33
/gene="IL6R"
/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details recorded"

Region 34..37
/gene="IL6R"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"

Region 39..>96
/gene="IL6R"
/region_name="Immunoglobulin like"
/note="IG_like"
/db_xref="CDD:5322"

Region 39..40
/gene="IL6R"
/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details recorded"

Region 43..46
/gene="IL6R"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"

Bond bond(47,96)
/gene="IL6R"
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/experiment="experimental evidence, no additional details recorded"

Region 48..49
/gene="IL6R"
/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details recorded"

Region 50
/gene="IL6R"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"

Region 52..53
/gene="IL6R"
/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details recorded"

Site 55
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/site_type="glycosylation"
/experiment="experimental evidence, no additional details recorded"
/note="N-linked (GlcNAc...)."

Region 56..63
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/experiment="experimental evidence, no additional details recorded"

Region 65..68
/gene="IL6R"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"

Region 72..83
/gene="IL6R"
/region_name="Beta-strand region"

Region /experiment="experimental evidence, no additional details recorded"
85
/gene="IL6R"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"

Region 88..90
/gene="IL6R"
/region_name="Helical region"
/experiment="experimental evidence, no additional details recorded"

Region 92..101
/gene="IL6R"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"

Site 93
/gene="IL6R"
/site_type="glycosylation"
/experiment="experimental evidence, no additional details recorded"
/note="N-linked (GlcNAc...)."

Region 103
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/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"

Region 105..110
/gene="IL6R"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"

Region 120..125
/gene="IL6R"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"

Bond bond(121,132)
/gene="IL6R"
/bond_type="disulfide"
/experiment="experimental evidence, no additional details recorded"

Site 121
/gene="IL6R"
/site_type="mutagenized"
/experiment="experimental evidence, no additional details recorded"
/note="C->S: Complete loss of ligand-binding."

Site 122
/gene="IL6R"
/site_type="mutagenized"
/experiment="experimental evidence, no additional details recorded"
/note="F->A: No change of ligand-binding and IL6 signaling."

Region 126..127
/gene="IL6R"
/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details recorded"

Region 128
/gene="IL6R"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"

Region 130..134
/gene="IL6R"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"

Site 132
/gene="IL6R"
/site_type="mutagenized"
/experiment="experimental evidence, no additional details recorded"
/note="C->A: Complete loss of ligand-binding."

Site 134
/gene="IL6R"
/site_type="mutagenized"
/experiment="experimental evidence, no additional details recorded"
/note="W->L: Complete loss of ligand-binding."

Region 137..138
/gene="IL6R"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"

Site 140
/gene="IL6R"
/site_type="mutagenized"
/experiment="experimental evidence, no additional details recorded"
/note="P->G: No change of ligand-binding and IL6 signaling."

Region 142..143
/gene="IL6R"
/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details recorded"

Region 145..157
/gene="IL6R"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"

Site 153
/gene="IL6R"
/site_type="mutagenized"
/experiment="experimental evidence, no additional details recorded"
/note="F->L: No change of ligand-binding and IL6 signaling."

Region 159..168
/gene="IL6R"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"

Bond bond(165,176)
/gene="IL6R"
/bond_type="disulfide"
/experiment="experimental evidence, no additional details recorded"

Site 165
/gene="IL6R"
/site_type="mutagenized"
/experiment="experimental evidence, no additional details recorded"
/note="C->L: Complete loss of ligand-binding."

Region 169..172
/gene="IL6R"
/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details recorded"

Region 173..178
/gene="IL6R"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"

Site 174
/gene="IL6R"
/site_type="mutagenized"
/experiment="experimental evidence, no additional details recorded"
/note="F->L: No change of ligand-binding and IL6 signaling."

Site 176
/gene="IL6R"
/site_type="mutagenized"
/experiment="experimental evidence, no additional details recorded"
/note="C->A: Complete loss of ligand-binding."

Region 182..183
/gene="IL6R"
/region_name="Hydrogen bonded turn"

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/experiment="experimental evidence, no additional details
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Site 184
/gene="IL6R"
/site_type="mutagenized"
/experiment="experimental evidence, no additional details
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/note="D->T: 30% decrease of ligand-binding and IL6
signaling."
Region 187..196
/gene="IL6R"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details
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Site 190
/gene="IL6R"
/site_type="mutagenized"
/experiment="experimental evidence, no additional details
recorded"
/note="V->G: 80% decrease of ligand-binding and no IL6
signaling."
Site 193
/gene="IL6R"
/site_type="mutagenized"
/experiment="experimental evidence, no additional details
recorded"
/note="C->D: Complete loss of ligand-binding."
Region 197..198
/gene="IL6R"
/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details
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Region 199..202
/gene="IL6R"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details
recorded"
Region 206..209
/gene="IL6R"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details
recorded"
Region 210..212
/gene="IL6R"
/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details
recorded"
Region 210
/gene="IL6R"
/region_name="Conflict"
/experiment="experimental evidence, no additional details
recorded"
/note="G -> D (in Ref. 4)."
Site 211
/gene="IL6R"
/site_type="mutagenized"
/experiment="experimental evidence, no additional details
recorded"
/note="C->A: No change of ligand-binding and IL6
signaling."
Region 214
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/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details
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Region 216..311
/gene="IL6R"
/region_name="Domain"
/experiment="experimental evidence, no additional details
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/note="Fibronectin type-III."
Region 216..308
/gene="IL6R"
/region_name="Fibronectin type 3 domain"
/note="FN3"
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Site 217

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Region 220..226
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Site 221
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Region 228..229
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Region 231..232
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Site 232
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/region 233
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/site 233
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/experiment="experimental evidence, no additional details recorded"
/region 234..239
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/experiment="experimental evidence, no additional details recorded"
Region 242..243
/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details recorded"
Site 245
/site_type="glycosylation"
/experiment="experimental evidence, no additional details recorded"
/region 247..249
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"
Region 251..259
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"
Site 254
/site_type="mutagenized"
/experiment="experimental evidence, no additional details recorded"
/region 260..261
/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details recorded"

Region recorded"
 263
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 /experiment="experimental evidence, no additional details
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Region 266..269
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 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
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Region 271..273
 /gene="IL6R"
 /region_name="Helical region"
 /experiment="experimental evidence, no additional details
 recorded"
Region 275..281
 /gene="IL6R"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
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Site 277
 /gene="IL6R"
 /site_type="mutagenized"
 /experiment="experimental evidence, no additional details
 recorded"
 /note="C->D: 30% increase of ligand-binding and 100%
 increase in IL6 signaling."
Site 278
 /gene="IL6R"
 /site_type="mutagenized"
 /experiment="experimental evidence, no additional details
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 /note="V->N: 50% Decrease of ligand-binding and 50%
 increase in IL6 signaling."
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 /note="I->D: Complete loss of ligand-binding."
Site 280
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 /experiment="experimental evidence, no additional details
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 /note="H->I: No change of ligand-binding and no IL6
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Site 281
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 /site_type="mutagenized"
 /experiment="experimental evidence, no additional details
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 /note="D->G: 70% decrease of ligand-binding and no IL6
 signaling."
Region 284..285
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Site 285
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 /site_type="mutagenized"
 /experiment="experimental evidence, no additional details
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 /note="G->D: 80% decrease of ligand-binding and no IL6
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Region 288..296
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 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
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Site 291
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 /site_type="mutagenized"
 /experiment="experimental evidence, no additional details
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/note="Q->K: Complete loss of ligand-binding."
Site 293
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 /site_type="mutagenized"
 /experiment="experimental evidence, no additional details recorded"
 /note="R->G: Complete loss of ligand-binding."
Region 297..299
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 /region_name="Hydrogen bonded turn"
 /experiment="experimental evidence, no additional details recorded"
Region 300..301
 /gene="IL6R"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details recorded"
Region 303..307
 /gene="IL6R"
 /region_name="Short sequence motif of biological interest"
 /experiment="experimental evidence, no additional details recorded"
 /note="WSXWS motif."
Region 310..312
 /gene="IL6R"
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 /experiment="experimental evidence, no additional details recorded"
Region 356..365
 /gene="IL6R"
 /region_name="Splicing variant"
 /experiment="experimental evidence, no additional details recorded"
 /note="VQDSSSVPLP -> GSRRRGSCGL (in isoform 2).
 /FTId=VSP_001682."
Region 358
 /gene="IL6R"
 /region_name="Variant"
 /experiment="experimental evidence, no additional details recorded"
 /note="D -> A (in dbSNP:8192284). /FTId=VAR_021995."
Region 366..468
 /gene="IL6R"
 /region_name="Splicing variant"
 /experiment="experimental evidence, no additional details recorded"
 /note="Missing (in isoform 2). /FTId=VSP_001683."
Region 366..386
 /gene="IL6R"
 /region_name="Transmembrane region"
 /inference="non-experimental evidence, no additional details recorded"
 /note="Potential."
Region 387..468
 /gene="IL6R"
 /region_name="Topological domain"
 /inference="non-experimental evidence, no additional details recorded"
 /note="Cytoplasmic (Potential)."

ORIGIN

```

1  mlavgcalla  allaapgaal  aprrcpagev  argvltslpg  dsvtltcpgv  epednatvhw
61  vlrkpaagsh  psrwagmrr  lllrsvqlhd  sgnyscyrag  rpagtvhllv  dvppeepqls
121 cfrksplsnv  vcewgprstp  slttkavllv  rkfqnspace  fgepcqysqe  sqkfscqlav
181 pegdssfyiv  smcvassvgs  kfsktqtfgg  cgilqpdppa  nitvtavarn  prwlsvtwqd
241 phswnsffyr  lrfelryrae  rsktfttmv  kdlqhhcvi  dawsglrhvv  qlraqeefgq
301 gewsewspea  mgtpwtesrs  ppaenevstp  mgalttnkdd  dnlfdrsan  atslpvqdss
361 svplptflva  ggslafgtll  ciaivlrffk  twklralkeg  ktsmhpypsl  gqlvperprp
421 tpvlvplisp  pvspsslgds  ntsshnrpda  rdprspydis  ntdyffpr

```

//

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Feb 1 2006 13:21:03